

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

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(A) NAME:

ASAT AG Applied Science & Technology

(B) STREET: Baarerstrasse 77

(C) CITY: Zug

(E) COUNTRY: Switzerland

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(F) POSTAL CODE: 6302

(ii) TITLE OF INVENTION: Recombinant antibodies

(iii) NUMBER OF SEQUENCES: 30

(iv) COMPUTER-READABLE FORM:

(A) MEDIUM TYPE: Floppy disk

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

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(D) SOFTWARE: PatentIn Release #1.0,
Version #1.30 (EPO)

(vi) ORIGINAL APPLICATION DATA:

(A) APPLICATION NUMBER: DE 19723904.8

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(B) APPLICATION DATE: 06-JUN-1997

(vi) ORIGINAL APPLICATION DATA:

(A) APPLICATION NUMBER: DE 19755227.7

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(B) APPLICATION DATE: 12-DEC-1997

(vi) ORIGINAL APPLICATION DATA:

(A) APPLICATION NUMBER: DE 19820663.1

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(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 357 base pairs

SECRET - ORIGINAL

- (B) TYPE: nucleotide
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5 (ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) NOTATION: 1..357

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

CAG GTG AAA CTG CTC GAG TCG GGC CCA GGA CTG GTG AAG CCT TCG GAG 48
 Gln Val Lys Leu Leu Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
 1 5 10 15

ACC CTG TCC CTC AAC TGC ACT GTC TCT GGT CGC TCC ATC AGT GGT TAC 96
 Thr Leu Ser Leu Asn Cys Thr Val Ser Gly Arg Ser Ile Ser Gly Tyr
 20 25 30

TCT TGG AGA TGG ATC CGG CAG TCT CCA GGG AAG GGA CTA GAG TGG ATT 144
 Ser Trp Arg Trp Ile Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Ile
 35 40 45

GGG GAT ATC TCT TAT AGT GGG AGT ACC AAG TAC AAA CCC TCC CTC AGG 192
 Gly Asp Ile Ser Tyr Ser Gly Ser Thr Lys Tyr Lys Pro Ser Leu Arg
 50 55 60

AGT CGA GTC ACC CTG TCA GTA GAC ACG TCC AAG AAC CAG TTC TCC CTG 240
 Ser Arg Val Thr Leu Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
 65 70 75 80

AAG CTG AAT TCG GTG ACC GCT GCG GAC ACG GCC GTC TAT TAC TGT GCG 288
 Lys Leu Asn Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95

CGA GTC TTG CCC TTT GAC CCG ATC TCG ATG GAC GTC TGG GGC AAA GGG 336
 Arg Val Leu Pro Phe Asp Pro Ile Ser Met Asp Val Trp Gly Lys Gly
 100 105 110

ACC ACG GTC ACC GTC TCC TCA 357
 Thr Thr Val Thr Val Ser Ser
 115

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 119 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Gln Val Lys Leu Leu Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
 1 5 10 15
 Thr Leu Ser Leu Asn Cys Thr Val Ser Gly Arg Ser Ile Ser Gly Tyr
 20 25 30
 Ser Trp Arg Trp Ile Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Ile
 35 40 45
 Gly Asp Ile Ser Tyr Ser Gly Ser Thr Lys Tyr Lys Pro Ser Leu Arg
 50 55 60
 Ser Arg Val Thr Leu Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
 65 70 75 80
 Lys Leu Asn Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95
 Arg Val Leu Pro Phe Asp Pro Ile Ser Met Asp Val Trp Gly Lys Gly
 100 105 110
 Thr Thr Val Thr Val Ser Ser
 115

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 base pairs
 (B) TYPE: nucleotide
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 1..333

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

GTG GTG ACT CAG CCA CCC TCA GCG TCT GGG ACC CCC GGG CAG TGG GTC 48
 Val Val Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln Trp Val
 120 125 130 135
 ACC ATC TCT TGT TCT GGG AGC AGC TCC AAC ATC AGA AGT AAT CCT GTT 96
 Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Arg Ser Asn Pro Val
 140 145 150
 AGC TGG TAT CAC CAG GTC CCA GGC ACG GCC CCC AAA CTC CTC ATC TTT 144
 Ser Trp Tyr His Gln Val Pro Gly Thr Ala Pro Lys Leu Leu Ile Phe
 155 160 165
 GGT AGT CAT CAG CGG CCC TCA GGG GTC CCT GAC CGA TTC TCT GGC TCC 192
 Gly Ser His Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser Gly Ser
 170 175 180
 AAG TCG GGC ACC TCC GCC TCC CTG GCC ATC CGT GGG CTC CAA TCT GGG 240
 Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Arg Gly Leu Gln Ser Gly
 185 190 195

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GAT GCT GGT GAC TAT TAC TGT GCA ACA TGG GAT GAC GGC CTC AAT GGT 288
 Asp Ala Gly Asp Tyr Tyr Cys Ala Thr Trp Asp Asp Gly Leu Asn Gly 215
 200 205 210
 CCG GTG TTC GGC GGA GGG ACC AAG CTG ACC GTC CTA AGT CAG CCC 333
 Pro Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Ser Gln Pro 230
 220 225 230

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

5

- (A) LENGTH: 111 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Val Val Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln Trp Val 15
 1 5 10
 Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Arg Ser Asn Pro Val 30
 20 25 30
 Ser Trp Tyr His Gln Val Pro Gly Thr Ala Pro Lys Leu Leu Ile Phe 45
 35 40 45
 Gly Ser His Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser Gly Ser 60
 50 55 60
 Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Arg Gly Leu Gln Ser Gly 80
 65 70 75 80
 Asp Ala Gly Asp Tyr Tyr Cys Ala Thr Trp Asp Asp Gly Leu Asn Gly 95
 85 90 95
 Pro Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Ser Gln Pro 110
 100 105 110

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 369 base pairs
 (B) TYPE: nucleotide
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 1..369

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

CAG GTG AAA CTG CTC GAG TCT GGG GGA GGC GTG GTC CAG CCT GGG AGG 48
 Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 115 120 125
 TCC CTG AGA CTC TCC TGT GCA GCC TCT GGA TTC ACC TTC AGT AGC TAT 96
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 130 135 140
 GCT ATG CAC TGG GTC CGC CAG GCT CCA GGC AAG GGG CTG GAG TGG GTG 144
 Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 145 150 155
 GCA GTT ATA TCA TAT GAT GGA AGC AAT AAA TAC TAC GCA GAC TCC GTG 192
 Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
 160 165 170 175
 AAG GGC CGA TTC GCC ATC TCC AGA GAC AAT TCC AAG AAC ACG CTG TAT 240
 Lys Gly Arg Phe Ala Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 180 185 190
 CTG CAA ATG AAC AGC CTG AGA GCT GAG GAC ACG GCT GTG TAT TAC TGT 288
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 195 200 205
 GCG AGA GCG CTG GGG AGC TGG GGG GGT TGG GAC CAC TAC ATG GAC GTC 336
 Ala Arg Ala Leu Gly Ser Trp Gly Gly Trp Asp His Tyr Met Asp Val
 210 215 220
 TGG GGC AAA GGG ACC ACG GTC ACC GTC TCC TCA 369
 Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
 225 230

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30
 Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Ala Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Ala Leu Gly Ser Trp Gly Gly Trp Asp His Tyr Met Asp Val
 100 105 110
 Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
 115 120

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 base pairs
 (B) TYPE: nucleotide
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 1..333

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

GTG GTG ACT CAG CCA CCC TCA GCG TCT GGG ACC CCC GGG CAG AGG GTC 48
 Val Val Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln Arg Val
 125 130 135

ACC ATC TCT TGT TCT GGA AGC AGC TCC AAC ATC GGA AGT AAT ACT GTA 96
 Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn Thr Val
 140 145 150 155

AAC TGG TAC CAG CAG CTC CCA GGA ACG GCC CCC AAA CTC CTC ATC TAT 144
 Asn Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr
 160 165 170

AGT AAT AAT CAG CGG CCC TCA GGG GTC CCT GAC CGA TTC TCT GGC TCC 192
 Ser Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser Gly Ser
 175 180 185

AAG TCT GGC ACC TCA GCC TCC CTG GCC ATC AGT GGG CTC CAG TCT GAG 240
 Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln Ser Glu
 190 195 200

GAT GAG GCT GAT TAT TAC TGT GCA GCA TGG GAT GAC AGC CTG AAT GGT 288
 Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu Asn Gly
 205 210 215

TGG GTG TTC GGC GGA GGG ACC AAG CTG ACC GTC CTA GGT CAG CCC 333
 Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln Pro
 220 225 230

15 (2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

- 55 -

Val Val Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln Arg Val
 1 5 10 15
 Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn Thr Val
 20 25 30
 Asn Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr
 35 40 45
 Ser Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser Gly Ser
 50 55 60
 Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln Ser Glu
 65 70 75 80
 Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu Asn Gly
 85 90 95
 Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln Pro
 100 105 110

(2) INFORMATION FOR SEQ ID NO: 9:

- 5 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 369 base pairs
 - (B) TYPE: nucleotide
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

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- (ix) FEATURE:
- (A) NAME/KEY: CDS
 - (B) LOCATION: 1..369

- 15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

CAG GTG AAA CTG CTC GAG TCT GGG GGA GGC TTG GTT CAC CCC GGG GGG	48
Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Leu Val His Pro Gly Gly	
115 120 125	
TCC CTG AGA CTC TCT TGT GCA GCC TCT GGA TTT ACG TTT GAC AAC TTT	96
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asn Phe	
130 135 140	
GCC ATG AGC TGG GTC CGC CAG GCT CCA GGG AAG GGG CTG GAG TGG GTC	144
Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val	
145 150 155	
TCA GGC ATT AGT GGT GGT CTT TTG ACA CAC TAC GCA GAC TCC GTG	192
Ser Gly Ile Ser Gly Gly Gly Leu Leu Thr His Tyr Ala Asp Ser Val	
160 165 170 175	
AAG GGC CGG TTC ACC ATC TCC AGA AAC AAT TCC AGG AAC ACT GTA TAC	240
Lys Gly Arg Phe Thr Ile Ser Arg Asn Asn Ser Arg Asn Thr Val Tyr	
180 185 190	
CTA CAA ATG AAC AGC CTG AGA GCC GAA GAC ACG GCC GTG TAT TAT TGT	288
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys	
195 200 205	

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GTG AGA GAT CTG GGC TAT AGA GTA CTT TCG ACT TTT ACT TTT GAT ATC 336
 Val Arg Asp Leu Gly Tyr Arg Val Leu Ser Thr Phe Thr Phe Asp Ile
 210 215 220

TGG GGC CAG GGG ACA AAG GTC ACC GTC TCT TCA 369
 Trp Gly Gln Gly Thr Lys Val Thr Val Ser Ser
 225 230

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 123 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Leu Val His Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asn Phe
 20 25 30
 Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Gly Ile Ser Gly Gly Gly Leu Leu Thr His Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asn Asn Ser Arg Asn Thr Val Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Val Arg Asp Leu Gly Tyr Arg Val Leu Ser Thr Phe Thr Phe Asp Ile
 100 105 110
 Trp Gly Gln Gly Thr Lys Val Thr Val Ser Ser
 115 120

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 375 base pairs
 (B) TYPE: nucleotide
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 1..375

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

GTG	GTG	ACT	CAG	CCT	GCC	TCC	GTG	TCT	GGG	TCT	CCT	GGA	CAG	TCG	ATC	48
Val	Val	Thr	Gln	Pro	Ala	Ser	Val	Ser	Gly	Ser	Pro	Gly	Gln	Ser	Ile	
125						130					135					
ACC	ATC	TCC	TGC	ACT	GGA	ACC	AGC	AGT	GCT	ATT	GGG	AAT	TAT	AAC	TTT	96
Thr	Ile	Ser	Cys	Thr	Gly	Thr	Ser	Ser	Ala	Ile	Gly	Asn	Tyr	Asn	Phe	
140					145				150						155	
GTC	CCC	TGG	TAC	CAA	CAG	CAC	CCA	GGC	AAA	GCC	CCC	AAA	CTC	ATG	ATT	144
Val	Pro	Trp	Tyr	Gln	Gln	His	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Met	Ile	
				160					165					170		
TAT	GAG	GGC	AGT	AAG	CGG	CCC	TCA	GGG	GTT	TCT	AAT	CGC	TTC	TCT	GGC	192
Tyr	Glu	Gly	Ser	Lys	Arg	Pro	Ser	Gly	Val	Ser	Asn	Arg	Phe	Ser	Gly	
			175					180					185			
TCC	AAG	TCT	GGC	AAC	ACG	GCC	TCC	CTG	ACA	ATC	TCT	GGG	CTC	CAG	GCT	240
Ser	Lys	Ser	Gly	Asn	Thr	Ala	Ser	Leu	Thr	Ile	Ser	Gly	Leu	Gln	Ala	
			190				195					200				
GAG	GAC	GAG	GCT	GAG	TAT	TAC	TGC	TGC	TCA	TAT	GTT	CAT	AGT	AGC	ACT	288
Glu	Asp	Glu	Ala	Glu	Tyr	Tyr	Cys	Cys	Ser	Tyr	Val	His	Ser	Ser	Thr	
	205					210					215					
AAT	TGG	GTG	TTC	GGC	GGA	GGG	ACC	AAG	CTG	ACC	GTC	CTA	GGT	CAG	CCC	336
Asn	Trp	Val	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Thr	Val	Leu	Gly	Gln	Pro	
						225					230				235	
AAG	GCT	GCC	CCC	TCG	GTC	ACT	CTG	TTC	CCA	CCC	TCC	TCT				375
Lys	Ala	Ala	Pro	Ser	Val	Thr	Leu	Phe	Pro	Pro	Ser	Ser				
				240					245							

5 (2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 125 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Val	Val	Thr	Gln	Pro	Ala	Ser	Val	Ser	Gly	Ser	Pro	Gly	Gln	Ser	Ile
1				5					10					15	
Thr	Ile	Ser	Cys	Thr	Gly	Thr	Ser	Ser	Ala	Ile	Gly	Asn	Tyr	Asn	Phe
			20					25					30		
Val	Pro	Trp	Tyr	Gln	Gln	His	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Met	Ile
		35					40					45			
Tyr	Glu	Gly	Ser	Lys	Arg	Pro	Ser	Gly	Val	Ser	Asn	Arg	Phe	Ser	Gly
	50					55					60				
Ser	Lys	Ser	Gly	Asn	Thr	Ala	Ser	Leu	Thr	Ile	Ser	Gly	Leu	Gln	Ala
	65				70					75				80	
Glu	Asp	Glu	Ala	Glu	Tyr	Tyr	Cys	Cys	Ser	Tyr	Val	His	Ser	Ser	Thr
				85					90					95	

Asn Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln Pro
 100 105 110
 Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser
 115 120 125

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 366 base pairs
 (B) TYPE: nucleotide
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10 (ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 1..366

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

15 CAG GTG AAA CTG CTC GAG TCA GGA CCA GGA CTG GTG AAG CCC TCG GAG 48
 Gln Val Lys Leu Leu Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
 130 135 140
 ACC CTG TCT CTC ACC TGC ACT GTC TCT GAT GTC TCC ATC AGA AGT CAT 96
 Thr Leu Ser Leu Thr Cys Thr Val Ser Asp Val Ser Ile Arg Ser His
 145 150 155
 TAC TGG AGT TGG CTC CGG CAG CCC CCA GGG AAG GGA CTG GAG TGG ATT 144
 Tyr Trp Ser Trp Leu Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
 160 165 170
 GGG TTT ATC TAT GAC GGT GCG AGA ACC AGG TTC AAC CCC TCC CTC AGG 192
 Gly Phe Ile Tyr Asp Gly Ala Arg Thr Arg Phe Asn Pro Ser Leu Arg
 175 180 185
 AGT CGA GTC TCC CTT TCA ATG GAC CCA TCC AAG AAG CAG TTT TCC CTG 240
 Ser Arg Val Ser Leu Ser Met Asp Pro Ser Lys Lys Gln Phe Ser Leu
 190 195 200 205
 AAA CTG GGG TCT GTG ACC GCT GCG GAC TCG GCC GTC TAC TAC TGT GCG 288
 Lys Leu Gly Ser Val Thr Ala Ala Asp Ser Ala Val Tyr Tyr Cys Ala
 210 215 220
 AGA GAC GCG GAT GGA GAT GGC TTC AGC CCA TAC TAC TTT CCC TAC TGG 336
 Arg Asp Ala Asp Gly Asp Gly Phe Ser Pro Tyr Tyr Phe Pro Tyr Trp
 225 230 235
 GGC CAG GGA ATC CCG GTC TCC GTC TCC TCG 366
 Gly Gln Gly Ile Pro Val Ser Val Ser Ser
 240 245

(2) INFORMATION FOR SEQ ID NO: 14

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 122 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Gln Val Lys Leu Leu Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
 1 5 10 15
 Thr Leu Ser Leu Thr Cys Thr Val Ser Asp Val Ser Ile Arg Ser His
 20 25 30
 Tyr Trp Ser Trp Leu Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
 35 40 45
 Gly Phe Ile Tyr Asp Gly Ala Arg Thr Arg Phe Asn Pro Ser Leu Arg
 50 55 60
 Ser Arg Val Ser Leu Ser Met Asp Pro Ser Lys Lys Gln Phe Ser Leu
 65 70 75 80
 Lys Leu Gly Ser Val Thr Ala Ala Asp Ser Ala Val Tyr Tyr Cys Ala
 85 90 95
 Arg Asp Ala Asp Gly Asp Gly Phe Ser Pro Tyr Tyr Phe Pro Tyr Trp
 100 105 110
 Gly Gln Gly Ile Pro Val Ser Val Ser Ser
 115 120

5 (2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 base pairs
 (B) TYPE: nucleotide
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 1..372

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

CAG GTG AAA CTG CTC GAG TCT GGG GGA GGC GTG GTC CAC CCT GGG AGG 48
 Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val His Pro Gly Arg
 125 130 135
 TCC CTG AGA CTC TCC TGT GCA GCC TCT GGA TTC ACC TTC AGT AGC TAT 96
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 140 145 150
 ACT ATG CAC TGG GTC CGC CAG GCT CCA GGC AAG GGG CTG GAG TGG GTG 144
 Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 155 160 165 170
 GCA CTT ATA TCA TAT GAT GGA AGC AAT AAA TAC TAC GCA GAC TCC GTC 192
 Ala Leu Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
 175 180 185

- 60 -

AAG GGC CGA TTC GCC ATC TCC AGA GAC AAT TCC AAG AAC ACG CTA TAT	240
Lys Gly Arg Phe Ala Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr	
190 195 200	
CTG CAA ATG AAC AGC CTG AGA GCT GAG GAC ACG GCT GTG TAT TAC TGT	288
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys	
205 210 215	
GCG AAA GAT GGC CGG AGT GGG AGC TAC GCC AGG TTC GAC GGT ATG GAC	336
Ala Lys Asp Gly Arg Ser Gly Ser Tyr Ala Arg Phe Asp Gly Met Asp	
220 225 230	
GTC TGG GGC CAA GGG ACC ACG GTC ACC GTC TCC TCA	372
Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser	
235 240 245	

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

5

- (A) LENGTH: 124 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val His Pro Gly Arg	15
1 5 10	
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr	30
20 25 30	
Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val	45
35 40 45	
Ala Leu Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val	60
50 55 60	
Lys Gly Arg Phe Ala Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr	80
65 70 75 80	
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys	95
85 90 95	
Ala Lys Asp Gly Arg Ser Gly Ser Tyr Ala Arg Phe Asp Gly Met Asp	110
100 105 110	
Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser	
115 120	

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 372 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..372

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

CAG GTG AAA CTG CTC GAG TCT GGG GGA GGC TTG GTA CAG CCT GGC AGG	48
Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg	
125 130 135 140	
TCC CTG AGA CTC TCC TGT GCA GCC TCT GGA TTC ACC TTT GAT GAT TAT	96
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr	
145 150 155	
GCC CTG CAC TGG GTC CGT CAA GCT CCA GGG AAG GGC CTG GAG TGG GTC	144
Ala Leu His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val	
160 165 170	
TCA GGT ATT AGT TGG GAT AGT GGT ACC ATA GGC TAT GCG GAC TCT GTG	192
Ser Gly Ile Ser Trp Asp Ser Gly Thr Ile Gly Tyr Ala Asp Ser Val	
175 180 185	
AAG GGC CGA TTC ACC ATC TCC AGA GAC AAC GCC AAG AAC TCC CTG TAT	240
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr	
190 195 200	
CTG CAA ATG AAC AGT CTG AGA GCT GAG GAC ACG GCC TTG TAT TAC TGT	288
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys	
205 210 215 220	
GTA AAA GAT ATG GGG TCT TCG GTA GTG GCT ACG TAC AAT GCT TTT GAT	336
Val Lys Asp Met Gly Ser Ser Val Val Ala Thr Tyr Asn Ala Phe Asp	
225 230 235	
ATC TGG GGC CAA GGG ACA ATG GTC ACC GTC TCT TCA	372
Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser	
240 245	

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 124 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg	
1 5 10 15	
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr	
20 25 30	
Ala Leu His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val	
35 40 45	
Ser Gly Ile Ser Trp Asp Ser Gly Thr Ile Gly Tyr Ala Asp Ser Val	
50 55 60	
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr	
65 70 75 80	

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Val Lys Asp Met Gly Ser Ser Val Val Ala Thr Tyr Asn Ala Phe Asp
100 105 110

Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
115 120

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

5 (A) LENGTH: 360 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: cDNA for mRNA

(vii) IMMEDIATE SOURCE:

(B) CLONE (E) : AI-X2

15 (ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 1..360

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

CAG GTG AAA CTG CTC GAG TCA GGC CCA GGA CTG GTG AAG CCT TCG GAG
Gln Val Lys Leu Leu Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu 48
125 130 135 140

ACC CTG TCC CTC ACC TGC ACT GTC TCT GGT GGC TCC TTC AGT ACT TAC 96
Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Phe Ser Thr Tyr
145 150 155

TAT TGG AGC TGG ATC CGG CAG CCC CCA GGG AAG GGA CTG GAG TGG ATT
Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile 144
160 165 170

GGG TAT ATC TAT TAC AGT GGG AAC ACC AAC TAC AAC CCC TCC CTC AAG 192
Gly Tyr Ile Tyr Tyr Ser Gly Asn Thr Asn Tyr Asn Pro Ser Leu Lys
175 180 195

AGT CGA GCC ACC ATA TCA GTA GAC ACG TCC AAG AAC CAG TTC TCC CTG 240
Ser Arg Ala Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
130 195 200

AAG CTG AGC TCT GTT ACC GCC GCA GAC ACG GCC GTA TAT TAC TGT GCG 288
Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
205 210 215 220

AGA CTG CGT AAC GAT GGC TGG AAT GAT GGC TTT GAT ATC TGG GGC CAA 336
Arg Leu Arg Asn Asp Gly Trp Asn Asp Gly Phe Asp Ile Trp Gly Gln
225 230 235

GGG ACA ATG GTC ACC GTC TCT TCA
 Gly Thr Met Val Thr Val Ser Ser
 240

360

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 120 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

Gln Val Lys Leu Leu Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
 1 5 10 15
 Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Phe Ser Thr Tyr
 20 25 30
 Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
 35 40 45
 Gly Tyr Ile Tyr Tyr Ser Gly Asn Thr Asn Tyr Asn Pro Ser Leu Lys
 50 55 60
 Ser Arg Ala Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
 65 70 75 80
 Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95
 Arg Leu Arg Asn Asp Gly Trp Asn Asp Gly Phe Asp Ile Trp Gly Gln
 100 105 110
 Gly Thr Met Val Thr Val Ser Ser
 115 120

(2) INFORMATION FOR SEQ ID NO: 21

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 369 base pairs
 (B) TYPE: nucleotide
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: cDNA for mRNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

25 (vii) IMMEDIATE SOURCE:

(B) CLONE(E): AI-B14

(viii) POSITION IN THE GENOME:

(A) CHROMOSOME/SEGMENT: 14

5

(B) MAP POSITION: q32.3

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..369

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

CAG GTG AAA CTG CTC GAG TCT GGG GGA GGC GTG GTC CAG CCT GGG AGG	48
Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Gln Pro Gly Arg	
125 130 135	
TCC CTG AGA CTC TCC TGT GCA GCC TCT GGA TTC ACC TTC AGT GAC TAT	96
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr	
140 145 150	
GGC ATG CAC TGG GTC CGC CAG GCT CCA GGC AAG GGG CTG GAG TGG GTG	144
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val	
155 160 165	
GCA GCT ATA TCA TAT GAT GGA AGT AAC AAA TAC TAT GCA GAC TCC GTG	192
Ala Ala Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val	
170 175 180	
AAG GGC CGA TTC TCC ATC TCC AGA GAC AAT TCC AAC AAT ACG CTA TAT	240
Lys Gly Arg Phe Ser Ile Ser Arg Asp Asn Ser Asn Asn Thr Leu Tyr	
185 190 195 200	
CTG CAA ATG AGC ACC CTG AGA GCT GAG GAC ACG GCT GTC TAT TTC TGT	288
Leu Gln Met Ser Thr Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe Cys	
205 210 215	
GCG AGA GAT TCG GAA ACG GCA ATA GCG GCA GCT GGA CGG TTT GAT ATC	336
Ala Arg Asp Ser Glu Thr Ala Ile Ala Ala Ala Gly Arg Phe Asp Ile	
220 225 230	
TGG GGC CAA GGG ACA ATG GTC ACC GTC TCT TCA	369
Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser	
235 240	

(2) INFORMATION FOR SEQ ID NO: 22:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 123 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
 20 25 30
 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ala Ala Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Ser Ile Ser Arg Asp Asn Ser Asn Asn Thr Leu Tyr
 65 70 75 80
 Leu Gln Met Ser Thr Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe Cys
 85 90 95
 Ala Arg Asp Ser Glu Thr Ala Ile Ala Ala Ala Gly Arg Phe Asp Ile
 100 105 110
 Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
 115 120

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:

- 5
- (A) LENGTH: 366 base pairs
 - (B) TYPE: nucleotide
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: cDNA for mRNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

15 (vii) IMMEDIATE SOURCE:

- (B) CLONE(E): AI-B18

(viii) POSITION IN THE GENOME:

- 20
- (A) CHROMOSOME/SEGMENT: 14
 - (B) MAP POSITION: q32.3

(ix) FEATURE:

- 25
- (A) NAME/KEY: CDS
 - (B) LOCATION: 1..366

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

CAG	GTG	AAA	CTG	CTC	GAG	GCG	GCT	GAG	GTG	AAG	AAG	CCT	GGG	TCC	
Gln	Val	Lys	Leu	Leu	Glu	Ser	Gly	Ala	Glu	Val	Lys	Pro	Gly	Ser	48
125						130				135					
TCG	GTG	ATG	GTC	TCC	TGC	AAG	GCT	TCT	GGA	GGC	ACC	TTC	AGC	CAT	
Ser	Val	Met	Val	Ser	Cys	Lys	Ala	Ser	Gly	Gly	Thr	Phe	Ser	His	96
140					145				150					155	
ACT	ATC	AGC	TGG	GTG	CGG	CAG	GCC	CCT	GGA	CAA	GGC	CTT	GAG	TGG	ATG
Thr	Ile	Ser	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Met
				160					165					170	144
GGA	GGG	ATC	ACC	CCT	ATC	TTT	GGT	ACA	GTG	AAC	TAC	GCA	CAG	AAG	TTC
Gly	Gly	Ile	Thr	Pro	Ile	Phe	Gly	Thr	Val	Asn	Tyr	Ala	Gln	Lys	Phe
			175					180					185		192
CAG	GGC	AGA	GTC	ACC	ATT	ACC	GCG	GAC	GAA	CCC	ACG	AGC	ACA	GCC	TAC
Gln	Gly	Arg	Val	Thr	Ile	Thr	Ala	Asp	Glu	Pro	Thr	Ser	Thr	Ala	Tyr
		190					195					200			240
ATG	GAA	CTG	AGG	AGC	CTG	ACA	TCT	GAC	GAC	TCG	GGC	ATC	TAT	TAC	TGT
Met	Glu	Leu	Arg	Ser	Leu	Thr	Ser	Asp	Asp	Ser	Gly	Ile	Tyr	Tyr	Cys
	205					210					215				288
GCG	AGA	GAA	GAT	GGC	ACT	ACA	GTA	CCA	AGT	CAA	CCC	CTT	GAG	TTC	TGG
Ala	Arg	Glu	Asp	Gly	Thr	Thr	Val	Pro	Ser	Gln	Pro	Leu	Glu	Phe	Trp
220					225					230					336
GGC	CAG	GGA	ACC	CGG	GTC	ACC	GTC	TCC	TCT						
Gly	Gln	Gly	Thr	Arg	Val	Thr	Val	Ser	Ser						366
				240					245						

(2) INFORMATION FOR SEQ ID NO: 24

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

Gln	Val	Lys	Leu	Leu	Glu	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Ser
1				5					10					15	
Ser	Val	Met	Val	Ser	Cys	Lys	Ala	Ser	Gly	Gly	Thr	Phe	Ser	Ser	His
			20					25					30		
Thr	Ile	Ser	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Met
		35					40					45			
Gly	Gly	Ile	Thr	Pro	Ile	Phe	Gly	Thr	Val	Asn	Tyr	Ala	Gln	Lys	Phe
	50					55					60				
Gln	Gly	Arg	Val	Thr	Ile	Thr	Ala	Asp	Glu	Pro	Thr	Ser	Thr	Ala	Tyr
	65				70					75					80
Met	Glu	Leu	Arg	Ser	Leu	Thr	Ser	Asp	Asp	Ser	Gly	Ile	Tyr	Tyr	Cys
				85					90					95	
Ala	Arg	Glu	Asp	Gly	Thr	Thr	Val	Pro	Ser	Gln	Pro	Leu	Glu	Phe	Trp
			100					105					110		
Gly	Gln	Gly	Thr	Arg	Val	Thr	Val	Ser	Ser						
		115					120								

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 363 base pairs
 (B) TYPE: nucleotide
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA for mRNA

10

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(vii) IMMEDIATE SOURCE:

15

- (B) CLONE(E): AI-B24

(viii) POSITION IN THE GENOME:

20

- (A) CHROMOSOME/SEGMENT: 14
 (B) MAP POSITION: q32.3

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 1..363

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

CAG GTG AAA CTG CTC GAG TCT GGG GGA GGC TTG GTC CAG CCT GGG GGG	48
Gln Val Lys Leu Leu Glu Ser Gly Gly Leu Val Gln Pro Gly Gly	
125 130 135	
TCC CTG AGA CTC TCC TGT TCA GCC TCT GGA TTC ACC TTC AAT AAA TAT	96
Ser Leu Arg Leu Ser Cys Ser Ala Ser Gly Phe Thr Phe Asn Lys Tyr	
140 145 150	
GCA ATA CAC TGG GTC CGC CAG GCT CCA GGG AAG GGA CTG GAA TAT GTT	144
Ala Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Tyr Val	
155 160 165 170	
TCA GCT ATT AGT AGT AAT GGG GGT AAC ACA TAC TAC GCA GAC TCC GTG	192
Ser Ala Ile Ser Ser Asn Gly Gly Asn Thr Tyr Tyr Ala Asp Ser Val	
175 180 185	
AAG GGC AGA TTC ACC ATC TCC AGA GAC AAT TCC AAG AAC ACG GTG TAT	240
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Val Tyr	
190 195 200	
CTT CAA ATG AGC AGT CTG AGA GCT GAG GAC ACG GCT GTG TAT TAC TGT	288
Leu Gln Met Ser Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys	
205 210 215	
GTT AGA GGA AGT GGG AGC TAC TTA GGA TAC TAC TTT GAC TAC TGG GGC	336
Val Arg Gly Ser Gly Ser Tyr Leu Gly Tyr Tyr Phe Asp Tyr Trp Gly	
220 225 230	

CAG GGA ACC CTG GTC ACC GTC TCC TCA
 Gln Gly Thr Leu Val Thr Val Ser Ser
 235 240

363

(2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 121 base pairs
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ser Ala Ser Gly Phe Thr Phe Asn Lys Tyr
 20 25 30
 Ala Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Tyr Val
 35 40 45
 Ser Ala Ile Ser Ser Asn Gly Gly Asn Thr Tyr Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Val Tyr
 65 70 75 80
 Leu Gln Met Ser Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Val Arg Gly Ser Gly Ser Tyr Leu Gly Tyr Tyr Phe Asp Tyr Trp Gly
 100 105 110
 Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 366 base pairs
 (B) TYPE: nucleotide
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: cDNA for mRNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

25 (vii) IMMEDIATE SOURCE:

(B) CLONE(E): AI-B24

(viii) POSITION IN THE GENOME:

(A) CHROMOSOME/SEGMENT: 22

(B) MAP POSITION: q11

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..366

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

GTG GTG ACT CAG CCA CCC TCG GTG TCA GTG GCT CCA AGA CAG ACG GCC 48
Val Val Thr Gln Pro Pro Ser Val Ser Val Ala Pro Arg Gln Thr Ala
125 130 135

ACG ATT ACC TGT GGG GGA TAC AAG ATT GGA AGT AAA AGT GTC CAC TGG 96
Thr Ile Thr Cys Gly Gly Tyr Lys Ile Gly Ser Lys Ser Val His Trp
140 145 150

TAC CAA CAG AAG CCA GGC CAG GCC CCT GTA TTG GTC GTC TAT GAG GAT 144
Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Val Tyr Glu Asp
155 160 165

TCC TAC CGG CCC TCA GAG ATC CCT GAG CGA TTC TCT GGC TCC AAC TCT 192
Ser Tyr Arg Pro Ser Glu Ile Pro Glu Arg Phe Ser Gly Ser Asn Ser
170 175 180 185

GGG AAC ATG GCC ACC CTG ACC ATC ACC GGG GTC GAA GCC GGG GAT GAG 240
Gly Asn Met Ala Thr Leu Thr Ile Thr Gly Val Glu Ala Gly Asp Glu
190 195 200

GCC GAC TAC TAC TGT CAG GTG TGG GAT AAT ACT AAT GAT CAG ACG ATA 288
Ala Asp Tyr Tyr Cys Gln Val Trp Asp Asn Thr Asn Asp Gln Thr Ile
205 210 215

TTC GGC GGA GGG ACC AAG CTG ACC GTC CTA CGT CAG CCC AAG GCT GCC 336
Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Arg Gln Pro Lys Ala Ala
220 225 230

CCC TCG GTC ACT CTG TTC CCG CCC TCC TCT 366
Pro Ser Val Thr Leu Phe Pro Pro Ser Ser
235 240

15 (2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 122 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

Val Val Thr Gln Pro Pro Ser Val Ser Val Ala Pro Arg Gln Thr Ala
 1 5 10 15
 Thr Ile Thr Cys Gly Gly Tyr Lys Ile Gly Ser Lys Ser Val His Trp
 20 25 30
 Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Val Tyr Glu Asp
 35 40 45
 Ser Tyr Arg Pro Ser Glu Ile Pro Glu Arg Phe Ser Gly Ser Asn Ser
 50 55 60
 Gly Asn Met Ala Thr Leu Thr Ile Thr Gly Val Glu Ala Gly Asp Glu
 65 70 75 80
 Ala Asp Tyr Tyr Cys Gln Val Trp Asp Asn Thr Asn Asp Gln Thr Ile
 85 90 95
 Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Arg Gln Pro Lys Ala Ala
 100 105 110
 Pro Ser Val Thr Leu Phe Pro Pro Ser Ser
 115 120

(2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 366 base pairs
 (B) TYPE: nucleotide
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA for mRNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(vii) IMMEDIATE SOURCE:

- (B) CLONE(E): AI-B38

(viii) POSITION IN THE GENOME:

- (A) CHROMOSOME/SEGMENT: 14
 (B) MAP POSITION: q32.3

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 1..366

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

COLLEGE OF MEDICINE
 UNIVERSITY OF CALIFORNIA
 SAN FRANCISCO
 CA 94143-0700

CAG GTG AAA CTG CTC GAG TCT GGG GCT GAG GTG AAG AAG CCT GGG GCC 48
 Gln Val Lys Leu Leu Glu Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 125 130 135
 TCA GTG AAG GTC TCC TGC AAG GTT TCC GGA TAC ACC CTC ACT GAA TTA 96
 Ser Val Lys Val Ser Cys Lys Val Ser Gly Tyr Thr Leu Thr Glu Leu
 140 145 150
 TCC ATG CAC TGG GTG CGA CAG GCT CCT GGA AAA GGG CTT GAG TGG ATG 144
 Ser Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Met
 155 160 165 170
 GGA GGT TTT GAT CCT GAA GAT GGT GAA ACA ATC TAC GCA CAG AAA TTC 192
 Gly Gly Phe Asp Pro Glu Asp Gly Glu Thr Ile Tyr Ala Gln Lys Phe
 175 180 185
 CAG GGC AGA GTC ACC ATG ACC GAG GAC ACA TCT ACA GAC ACG GCC TAC 240
 Gln Gly Arg Val Thr Met Thr Glu Asp Thr Ser Thr Asp Thr Ala Tyr
 190 195 200
 ATG GAG CTG AGC AGC CTG AGA TCT GAG GAC ACG GCC GTG TAT TAC TGT 288
 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 205 210 215
 GAG ACA GGT CTG AGG TCG TAC AAC TAT GGT CGT AAC CTT GAC TAT TGG 336
 Glu Thr Gly Leu Arg Ser Tyr Asn Tyr Gly Arg Asn Leu Asp Tyr Trp
 220 225 230
 GGC CAG GGA ACC CTG GTC ACC GTC TCC TCA 366
 Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 235 240

(2) INFORMATION FOR SEQ ID NO: 30:

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

Gln Val Lys Leu Leu Glu Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15
 Ser Val Lys Val Ser Cys Lys Val Ser Gly Tyr Thr Leu Thr Glu Leu
 20 25 30
 Ser Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Met
 35 40 45
 Gly Gly Phe Asp Pro Glu Asp Gly Glu Thr Ile Tyr Ala Gln Lys Phe
 50 55 60
 Gln Gly Arg Val Thr Met Thr Glu Asp Thr Ser Thr Asp Thr Ala Tyr
 65 70 75 80
 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Glu Thr Gly Leu Arg Ser Tyr Asn Tyr Gly Arg Asn Leu Asp Tyr Trp
 100 105 110

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Year	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100
1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	